

SEQUENCE LISTING

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<120> TENEURIN C-TERMINAL ASSOCIATED PEPTIDES (TCAP) AND METHODS AND USES THEREOF

<130> 090931-360630

<140> US 10/510,959

<141> 2005-08-10

<150> PCT/CA03/00622

<151> 2003-05-02

<150> US 60/376,879

<151> 2002-05-02

<150> US 60/377,231

<151> 2002-05-03

<150> US 60/424,016

<151> 2002-11-06

<160> 138

<170> PatentIn version 3.1

<210> 1

<211> 1490

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout Ten M3 carboxy termini'

<400> 1

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aggatgccgg agatccagct gagccgccgg cgctccaacc gggagaaacc ctggctgtgg	120
ttcgccaccg ccaagtctct gatcggtaag ggtgtcatgt tggcggtgac gcagggccgt	180
gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggctgc cgccgtcctc	240
aacaatgcgt tctacctgga ggacctgcac ttcacgggtgg agggacgcga cacgcactac	300
ttcatcaaga ccagcctccc ggagagcgac ctgggagcgc tgaggctgac aagcgggagg	360
aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tggatgaacgg	420
cagaaccggc gcttcgccga cgtggagctg cagtacggcg ctctagcgct ccacgtgcgc	480

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tatggcatga ctctggacga ggagaaggcg cgtgtgctgg agcaggccag gcagaaggcg      540
ttgtcgagtg cctgggccag ggagcaacaa cgggtgaggg agggggagga gggggtgagg      600
ctgtggacgg agggggagaa gaggcagctg ctgagcggga ggaaggttct gggctacgac      660
gggtactacg tcctctccat agagcagtac cccgagctag cagactccgc taacaacatc      720
cagttcctca ggcagagcga aatagggaag aggtaacaga cagaatcctc ggcactggcc      780
gccaaagaga ctacccccctc caaatcctgc cccccaacct ccctcgctc ccccttttc      840
tctaaaaagg gggaggggtcc aggctagtgc tgtgttttagc gccgactagc tgaaacaaac      900
agtaaaatgt agaatatctt aaactgaact atacctaata ctaccactgt ggggcctgaa      960
aatcaaacaa aacggctcca actgacgcaa atgtttgtcc catgtgctat acagcgttga     1020
atggactgtg gactctcttg aaaagagaga aaaaaaagtc aaaactctcg gtttgtgaaa     1080
ggagaaaaaa acgttttttt tttttttaaa tagacttcct gaatttgctt tcggaaaaaa     1140
tattttaaaa agaaagaaga aatgtgttta catacgcata aactacaac acgtctggac     1200
taatagaaga aaagccttct ggtttcttac acaggacaac gtctataatc tgattctaca     1260
tcctgacgac tgacctttga ttgacctttg cgtactgaaa aaggtagtgt tgttgttcgc     1320
agtaggacca tgggtctcca atgggtgtaa ctagacagtt aaaaccactt gttgaaacca     1380
cttgcttggt cttctgcttt tctttccaaa agggacaaaa cagctccac caagtgactt     1440
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<210> 2

<211> 756

<212> DNA

<213> Artificial Sequence

<220>

<223> Rainbow Trout Ten M3 coding sequence of carboxy termini of Ten M3

<400> 2

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tccatctcgg gggtgcaaca ggaagtgacc cggcaagcca aggctttcct gtccttcgag      60
aggatgccgg agatccagct gagccgccgg cgctccaacc gggagaaacc ctggctgtgg     120
ttcgccaccg ccaagtctct gatcggtgta ggtgtcatgt tggcggtgac gcagggccgt     180
gtggtcacca acgctctgaa catcgccaac gaggactgca tcaaggtcgc cgccgtcctc     240
aacaatgcgt tctacctgga ggacctgcac ttcacgggtg agggacgcga cacgcactac     300
ttcatcaaga ccagcctccc ggagagcgac ctgggagcgc tgaggctgac aagcgggagg     360

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aagtcgctgg agaacggaag tcaacgtgac tgtgtcccag tccaccaccg tggatgaacgg      420
cagaaccggc gcttcgccga cgtggagctg cagtacggcg ctctagcgct ccacgtgcgc      480
tatggcatga ctctggacga ggagaaggcg cgtgtgctgg agcaggccag gcagaaggcg      540
ttgtcgagtg cctggtccag ggagcaacaa cgggtgaggg agggggagga gggggtgagg      600
ctgtggacgg agggggagaa gaggcagctg ctgagcggga ggaaggttct gggctacgac      660
gggtactacg tcctctccat agagcagtac cccgagctag cagactccgc taacaacatc      720
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<210> 3
<211> 251
<212> PRT
<213> Artificial Sequence

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<220>
<223> Rainbow Trout Ten M3 carboxy termini of Ten M3

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<400> 3

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Ser Ile Ser Gly Val Gln Gln Glu Val Thr Arg Gln Ala Lys Ala Phe
1              5              10              15

```

```

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser
          20              25              30

```

```

Asn Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Ala Lys Ser Leu Ile
          35              40              45

```

```

Gly Lys Gly Val Met Leu Ala Val Thr Gln Gly Arg Val Val Thr Asn
          50              55              60

```

```

Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
65              70              75              80

```

```

Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly Arg
          85              90              95

```

```

Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu Gly
          100             105             110

```

```

Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val Asn
          115             120             125

```

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
 130 135 140

Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val Arg
 145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln Ala
 165 170 175

Arg Gln Lys Ala Leu Ser Ser Ala Trp Ser Arg Glu Gln Gln Arg Val
 180 185 190

Arg Glu Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys Arg
 195 200 205

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
 210 215 220

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
 225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
 245 250

<210> 4
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse Ten M1

<400> 4

Met Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe
 1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Gln Tyr Asn Glu Gly Arg
 20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val
 35 40 45

5/77

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Glu Gly Ile Val Thr Ala
50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly
85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu
100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val
115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg
130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile
145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Met
165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Gln Glu Gln Arg Arg
180 185 190

Leu Gln Glu Gly Glu Glu Gly Thr Arg Val Trp Thr Glu Gly Glu Lys
195 200 205

Gln Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
210 215 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
245 250

<210> 5

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse Ten M2

<400> 5

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe
 1 5 10 15

Leu Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile
 20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly
 35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val
 50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn
 65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp
 85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ala Ala Asp Gly Asp Leu Val Thr
 100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val
 115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe
 130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr
 145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp
 165 170 175

Gln Ala Gly Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln
 180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu
 195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr
 210 215 220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser
 225 230 235 240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
 245 250

<210> 6
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse Ten M3

<400> 6

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe
 1 5 10 15

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Lys Ala
 20 25 30

Gly Ala Glu Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile
 35 40 45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn
 50 55 60

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
 65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys
 85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly
 100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn
 115 120 125

8/77

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg
145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala
165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val
180 185 190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg
195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
245 250

<210> 7
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> Mouse Ten M4

<400> 7

Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe
1 5 10 15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser
20 25 30

Cys Gln Gln Ala Pro Glu Thr Lys Lys Phe Ala Ser Ser Gly Ser Ile
35 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr
50 55 60

9/77

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Ile Ala Ala Ile
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly
85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu
100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val
115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Met Leu Ile Gln Leu Gln Tyr
130 135 140

Arg Ala Leu Cys Leu Asn Thr Arg Tyr Gly Thr Thr Val Asp Glu Glu
145 150 155 160

Lys Val Arg Val Leu Glu Leu Ala Arg Gln Arg Ala Val Arg Gln Ala
165 170 175

Trp Ala Arg Glu Gln Gln Arg Leu Arg Glu Gly Glu Glu Gly Leu Arg
180 185 190

Ala Trp Thr Asp Gly Glu Lys Gln Gln Val Leu Asn Thr Gly Arg Val
195 200 205

Gln Gly Tyr Asp Gly Phe Phe Val Thr Ser Val Glu Gln Tyr Pro Glu
210 215 220

Leu Ser Asp Ser Ala Asn Asn Ile His Phe Met Arg Gln Ser Glu Met
225 230 235 240

Gly Arg Arg

<210> 8

<211> 252

<212> PRT

<213> Artificial Sequence

<220>

10/77

<223> Human Ten M1

<400> 8

Thr Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe
1 5 10 15

Ile Ser Leu Asp Gln Leu Pro Met Thr Pro Arg Tyr Asn Asp Gly Arg
20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val
35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala
50 55 60

Asp Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile
65 70 75 80

Leu Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly
85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu
100 105 110

Val Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val
115 120 125

Asn Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg
130 135 140

Arg Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile
145 150 155 160

Arg Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Ile
165 170 175

Ala Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg
180 185 190

Leu Gln Glu Gly Glu Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys
195 200 205

11/77

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
210 215 220

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
245 250

<210> 9
<211> 253
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Ten M2

<400> 9

Leu Ile Thr Gly Val Gln Gln Thr Thr Glu Arg His Asn Gln Ala Phe
1 5 10 15

Met Ala Leu Glu Gly Gln Val Ile Thr Lys Lys Leu His Ala Ser Ile
20 25 30

Arg Glu Lys Ala Gly His Trp Phe Ala Thr Thr Thr Pro Ile Ile Gly
35 40 45

Lys Gly Ile Met Phe Ala Ile Lys Glu Gly Arg Val Thr Thr Gly Val
50 55 60

Ser Ser Ile Ala Ser Glu Asp Ser Arg Lys Val Ala Ser Val Leu Asn
65 70 75 80

Asn Ala Tyr Tyr Leu Asp Lys Met His Tyr Ser Ile Glu Gly Lys Asp
85 90 95

Thr His Tyr Phe Val Lys Ile Gly Ser Ala Asp Gly Asp Leu Val Thr
100 105 110

Leu Gly Thr Thr Ile Gly Arg Lys Val Leu Glu Ser Gly Val Asn Val
115 120 125

Thr Val Ser Gln Pro Thr Leu Leu Val Asn Gly Arg Thr Arg Arg Phe
130 135 140

Thr Asn Ile Glu Phe Gln Tyr Ser Thr Leu Leu Leu Ser Ile Arg Tyr
 145 150 155 160

Gly Leu Thr Pro Asp Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Asp
 165 170 175

Gln Ala Arg Gln Arg Ala Leu Gly Thr Ala Trp Ala Lys Glu Gln Gln
 180 185 190

Lys Ala Arg Asp Gly Arg Glu Gly Ser Arg Leu Trp Thr Glu Gly Glu
 195 200 205

Lys Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr
 210 215 220

Tyr Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser
 225 230 235 240

Asn Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
 245 250

<210> 10
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human Ten M3

<400> 10

Pro Ile Phe Gly Val Gln Gln Gln Val Ala Arg Gln Ala Lys Ala Phe
 1 5 10 15

Leu Ser Leu Gly Lys Met Ala Glu Val Gln Val Ser Arg Arg Arg Ala
 20 25 30

Gly Gly Ala Gln Ser Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile
 35 40 45

Gly Lys Gly Val Met Leu Ala Val Ser Gln Gly Arg Val Gln Thr Asn
 50 55 60

13/77

Val Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Ala Ala Val Leu
65 70 75 80

Asn Asn Ala Phe Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Lys
85 90 95

Asp Thr His Tyr Phe Ile Lys Thr Thr Thr Pro Glu Ser Asp Leu Gly
100 105 110

Thr Leu Arg Leu Thr Ser Gly Arg Lys Ala Leu Glu Asn Gly Ile Asn
115 120 125

Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg Arg
130 135 140

Phe Ala Asp Val Glu Met Gln Phe Gly Ala Leu Ala Leu His Val Arg
145 150 155 160

Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Ile Leu Glu Gln Ala
165 170 175

Arg Gln Arg Ala Leu Ala Arg Ala Trp Ala Arg Glu Gln Gln Arg Val
180 185 190

Arg Asp Gly Glu Glu Gly Ala Arg Leu Trp Thr Glu Gly Glu Lys Arg
195 200 205

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
210 215 220

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
225 230 235 240

Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
245 250

<210> 11
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> Human Ten M4

<400> 11

Ser Ile Leu Gly Val Gln Cys Glu Val Gln Lys Gln Leu Lys Ala Phe
 1 5 10 15

Val Thr Leu Glu Arg Phe Asp Gln Leu Tyr Gly Ser Thr Ile Thr Ser
 20 25 30

Cys Leu Gln Ala Pro Lys Thr Lys Lys Phe Ala Ser Ser Gly Ser Val
 35 40 45

Phe Gly Lys Gly Val Lys Phe Ala Leu Lys Asp Gly Arg Val Thr Thr
 50 55 60

Asp Ile Ile Ser Val Ala Asn Glu Asp Gly Arg Arg Val Ala Ala Ile
 65 70 75 80

Leu Asn His Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Asp Gly
 85 90 95

Val Asp Thr His Tyr Phe Val Lys Pro Gly Pro Ser Glu Gly Asp Leu
 100 105 110

Ala Ile Leu Gly Leu Ser Gly Gly Arg Arg Thr Leu Glu Asn Gly Val
 115 120 125

Asn Val Thr Val Ser Gln Ile Asn Thr Val Leu Ser Gly Arg Thr Arg
 130 135 140

Arg Tyr Thr Asp Ile Gln Leu Gln Tyr Gly Ala Leu Cys Leu Asn Thr
 145 150 155 160

Arg Tyr Gly Thr Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Leu
 165 170 175

Ala Arg Gln Arg Ala Val Arg Gln Ala Trp Ala Arg Glu Gln Gln Arg
 180 185 190

Leu Arg Glu Gly Glu Glu Gly Leu Arg Ala Trp Thr Glu Gly Glu Lys
 195 200 205

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
 210 215 220

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
 225 230 235 240

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
 245 250

<210> 12
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Zebrafish Ten M3

<400> 12

Ser Ile Ser Gly Val Gln Gln Glu Val Met Arg Gln Ala Lys Ala Phe
 1 5 10 15

Leu Ser Phe Glu Arg Met Pro Glu Ile Gln Leu Ser Arg Arg Arg Ser
 20 25 30

Ser Arg Glu Lys Pro Trp Leu Trp Phe Ala Thr Val Lys Ser Leu Ile
 35 40 45

Gly Lys Gly Val Met Leu Ala Ile Thr Ser Lys Gly Gln Val Ala Thr
 50 55 60

Asn Ala Leu Asn Ile Ala Asn Glu Asp Cys Ile Lys Val Val Thr Val
 65 70 75 80

Leu Asn Asn Ala Phe Tyr Leu Glu Asp Leu His Phe Thr Val Glu Gly
 85 90 95

Arg Asp Thr His Tyr Phe Ile Lys Thr Ser Leu Pro Glu Ser Asp Leu
 100 105 110

Gly Ala Leu Arg Leu Thr Ser Gly Arg Lys Ser Leu Glu Asn Gly Val
 115 120 125

Asn Val Thr Val Ser Gln Ser Thr Thr Val Val Asn Gly Arg Thr Arg
 130 135 140

16/77

Arg Phe Ala Asp Val Glu Leu Gln Tyr Gly Ala Leu Ala Leu His Val
145 150 155 160

Arg Tyr Gly Met Thr Leu Asp Glu Glu Lys Ala Arg Val Leu Glu Gln
165 170 175

Ala Arg Gln Arg Ala Leu Ser Ser Ala Trp Ala Arg Glu Gln Gln Arg
180 185 190

Val Arg Asp Gly Glu Glu Gly Val Arg Leu Trp Thr Glu Gly Glu Lys
195 200 205

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
210 215 220

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
225 230 235 240

Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
245 250

<210> 13
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Rainbow Trout TCAP3 (40a.a.)

<400> 13

Gln Leu Leu Ser Gly Arg Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15

Leu Ser Ile Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 14
<211> 41
<212> PRT
<213> Artificial Sequence

<220>

<223> Rainbow Trout TCAP 3 (41a.a.)

<400> 14

Arg	Gln	Leu	Leu	Ser	Gly	Arg	Lys	Val	Leu	Gly	Tyr	Asp	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Ser	Ile	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile
			35				40	

<210> 15

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (43 a.a.)

<400> 15

Gln	Leu	Leu	Ser	Gly	Arg	Lys	Val	Leu	Gly	Tyr	Asp	Gly	Tyr	Tyr	Val
1				5					10					15	

Leu	Ser	Ile	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn	Ile
			20					25					30		

Gln	Phe	Leu	Arg	Gln	Ser	Glu	Ile	Gly	Lys	Arg
			35				40			

<210> 16

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (44 a.a.)

<400> 16

Arg	Gln	Leu	Leu	Ser	Gly	Arg	Lys	Val	Leu	Gly	Tyr	Asp	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Ser	Ile	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
 35 40

<210> 17
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Rainbow Trout TCAP3 (120 n.a.)

<400> 17
 cagctgctga gcgggaggaa ggttctgggc tacgacgggt actacgtcct ctccatagag 60
 cagtacccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata 120

<210> 18
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Rainbow Trout TCAP3 (123 n.a.)

<400> 18
 aggcagctgc tgagcgggag gaaggttctg ggctacgacg ggtactacgt cctctccata 60
 gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa 120
 ata 123

<210> 19
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Rainbow Trout preTCAP3 (129 n.a.)

<400> 19
 cagctgctga gcgggaggaa ggttctgggc tacgacgggt actacgtcct ctccatagag 60
 cagtacccccg agctagcaga ctccgctaac aacatccagt tcctcaggca gagcgaaata 120
 gggaagagg 129

<210> 20
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Rainbow Trout preTCAP3 (132 n.a.)

<400> 20
aggcagctgc tgagcgggag gaaggttctg ggctacgacg ggtactacgt cctctccata 60
gagcagtacc ccgagctagc agactccgct aacaacatcc agttcctcag gcagagcgaa 120
atagggaga gg 132

<210> 21
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Zebrafish TCAP3 (40 a.a.)

<400> 21
Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15
Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val
20 25 30
Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 22
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Zebrafish TCAP3 (41 a.a.)

<400> 22
Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
1 5 10 15
Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
20 25 30
Val Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 23
<211> 43

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Zebrafish preTCAP3 (43 a.a.)

<400> 23

Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr Val
 1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Val
 20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
 35 40

<210> 24
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Zebrafish preTCAP3 (44 a.a.)

<400> 24

Arg Gln Leu Leu Ser Ser Gly Lys Val Leu Gly Tyr Asp Gly Tyr Tyr
 1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
 20 25 30

Val Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
 35 40

<210> 25
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Zebrafish TCAP3 (120 n.a.)

<400> 25
 cagttgctca gctctgggaa ggtgctgggt tacgatgggt actatgtact atcagtgagg 60
 caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata 120

<210> 26
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Zebrafish TCAP3 (123 n.a.)

<400> 26
 aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg 60
 gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag 120
 ata 123

<210> 27
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Zebrafish TCAP3 (129 n.a.)

<400> 27
 cagttgctca gctctgggaa ggtgctgggt tacgatgggt actatgtact atcagtggag 60
 caataccctg aactggccga cagtgccaac aatgtccagt tcttgaggca gagtgagata 120
 gggaagagg 129

<210> 28
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Zebrafish preTCAP3 (132 n.a.)

<400> 28
 aggcagttgc tcagctctgg gaaggtgctg ggttacgatg gttactatgt actatcagtg 60
 gagcaatacc ctgaactggc cgacagtgcc aacaatgtcc agttcttgag gcagagtgag 120
 atagggaaga gg 132

<210> 29
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Zebrafish TCAP4 (40 a.a.)

<400> 29

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile
 1 5 10 15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val
 20 25 30

His Phe Trp Arg Gln Thr Glu Met
 35 40

<210> 30

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish TCAP4 (41 a.a.)

<400> 30

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
 1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
 20 25 30

Val His Phe Trp Arg Gln Thr Glu Met
 35 40

<210> 31

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Zebrafish preTCAP4 (43 a.a.)

<400> 31

Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr Ile
 1 5 10 15

Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn Val
 20 25 30

His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
 35 40

<210> 32
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Zebrafish preTCAP4 (44 a.a.)

<400> 32

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
 1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
 20 25 30

Val His Phe Trp Arg Gln Thr Glu Met Gly Arg Arg
 35 40

<210> 33
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Zebrafish TCAP4 (120 n.a.)

<400> 33
 cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac 60
 cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120

<210> 34
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Zebrafish TCAP4 (123 n.a.)

<400> 34
 cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc 60
 gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag 120
 atg 123

<210> 35
 <211> 129

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Zebrafish preTCAP4 (129 n.a.)

<400> 35
 cagctcctaa gctctggacg tgtacagggc tacgaaggct tctacatagt atcagtcgac 60
 cagttcccag agttgactga caacataaat aacgtccatt tctggcgaca gactgagatg 120
 ggacgcagg 129

<210> 36
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Zebrafish preTCAP4 (132 n.a.)

<400> 36
 cagcagctcc taagctctgg acgtgtacag ggctacgaag gcttctacat agtatcagtc 60
 gaccagttcc cagagttgac tgacaacata aataacgtcc atttctggcg acagactgag 120
 atgggacgca gg 132

<210> 37
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP1 (40 a.a.)

<400> 37

Gln Leu Leu Gly Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
 1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
 20 25 30

His Phe Met Arg Gln Ser Glu Ile
 35 40

<210> 38
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Mouse TCAP1 (41 a.a.)

<400> 38

Gln	Gln	Leu	Leu	Gly	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Phe
1				5					10					15	

Val	Leu	Ser	Val	Glu	Gln	Tyr	Leu	Glu	Leu	Ser	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile	His	Phe	Met	Arg	Gln	Ser	Glu	Ile
		35					40	

<210> 39

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (43 a.a.)

<400> 39

Gln	Leu	Leu	Gly	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Phe	Val
1				5					10					15	

Leu	Ser	Val	Glu	Gln	Tyr	Leu	Glu	Leu	Ser	Asp	Ser	Ala	Asn	Asn	Ile
			20					25					30		

His	Phe	Met	Arg	Gln	Ser	Glu	Ile	Gly	Arg	Arg
		35					40			

<210> 40

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (44 a.a.)

<400> 40

Gln	Gln	Leu	Leu	Gly	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Asp	Gly	Tyr	Phe
1				5					10					15	

Val	Leu	Ser	Val	Glu	Gln	Tyr	Leu	Glu	Leu	Ser	Asp	Ser	Ala	Asn	Asn
			20					25					30		

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
 35 40

<210> 41
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP1 (120 n.a.)

<400> 41
 cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag 60
 cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaaata 120

<210> 42
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP1 (123 n.a.)

<400> 42
 cagcagcttt tgggcaccgg gaggggtgcag gggatatgatg ggtattttgt cttgtctgtt 60
 gagcagtatt tagaactttc agacagtgcc aacaatattc acttcatgag acagagtgaa 120
 ata 123

<210> 43
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP1 (129 n.a.)

<400> 43
 cagcttttgg gcaccgggag ggtgcagggg tatgatgggt attttgtctt gtctgttgag 60
 cagtatttag aactttcaga cagtgccaac aatattcact tcatgagaca gagtgaaata 120
 ggcaggagg 129

<210> 44
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Mouse preTCAP1 (132 n.a.)

<400> 44

cagcagcttt tgggcaccgg gaggggtgcag gggatatgatg ggtattttgt cttgtctggt 60

gagcagtatt tagaactttc agacagtgcc aacaatatc acttcatgag acagagtgaa 120

ataggcagga gg 132

<210> 45

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP2 (40 a.a.)

<400> 45

Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr	Val
1				5				10					15		

Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn	Ile
			20					25					30		

Gln	Phe	Leu	Arg	Gln	Asn	Glu	Ile
		35				40	

<210> 46

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP2 (41 a.a.)

<400> 46

Gln	Gln	Leu	Leu	Ser	Thr	Gly	Arg	Val	Gln	Gly	Tyr	Glu	Gly	Tyr	Tyr
1				5					10					15	

Val	Leu	Pro	Val	Glu	Gln	Tyr	Pro	Glu	Leu	Ala	Asp	Ser	Ser	Ser	Asn
			20					25					30		

Ile	Gln	Phe	Leu	Arg	Gln	Asn	Glu	Met
			35				40	

<210> 47
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP2 (43 a.a)

<400> 47

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
 1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
 20 25 30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
 35 40

<210> 48
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP2 (44 a.a.)

<400> 48

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
 1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
 20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
 35 40

<210> 49
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP2 (120 n.a.)

<400> 49
 caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa 60
 cagtaccogg agctggcaga cagtagcagc aacatccagt tottaagaca gaatgagagg 120

<210> 50
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP 2 (123 n.a.)

<400> 50
 cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60
 gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag 120
 atg 123

<210> 51
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP2 (129 n.a.)

<400> 51
 caactcctga gcacgggacg ggtacaaggt tatgagggct attacgtact tccggtggaa 60
 cagtaccggg agctggcaga cagtagcagc aacatccagt tcttaagaca gaatgagatg 120
 ggaaagagg 129

<210> 52
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP2 (132 n.a.)

<400> 52
 cagcaactcc tgagcacggg acgggtacaa ggttatgagg gctattacgt acttccggtg 60
 gaacagtacc cggagctggc agacagtagc agcaacatcc agttcttaag acagaatgag 120
 atgggaaaga gg 132

<210> 53
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Mouse TCAP3 (40 a.a.)

<400> 53

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 54

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse TCAP3 (41 a..a)

<400> 54

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile
35 40

<210> 55

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Mouse preTCAP3 (43 a.a.)

<400> 55

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
 35 40

<210> 56
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP3 (44 a.a.)

<400> 56

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
 1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
 20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Lys Arg
 35 40

<210> 57
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP3 (120 n.a.)

<400> 57
 cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag 60
 cagtaccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc 120

<210> 58
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP3 (123 n.a.)

<400> 58
 cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcgggtg 60
 gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag 120
 atc 123

<210> 59
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP3 (129 n.a.)

<400> 59
 cagctgctga gcgctggcaa ggtgcagggc tacgatgggt actacgtact gtcggtggag 60
 cagtacccccg agctggctga cagtgccaac aacatccagt tcttgcgaca aagtgagatc 120
 ggcaagagg 129

<210> 60
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP3 (132 n.a.)

<400> 60
 cggcagctgc tgagcgctgg caaggtgcag ggctacgatg ggtactacgt actgtcggtg 60
 gagcagtacc ccgagctggc tgacagtgcc aacaacatcc agttcttgcg acaaagtgag 120
 atcggcaaga gg 132

<210> 61
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP4 (40 a.a.)

<400> 61

Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
 1 5 10 15

Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
 20 25 30

His Phe Met Arg Gln Ser Glu Met
 35 40

<210> 62
 <211> 41

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP4 (41 a.a.)

<400> 62

Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
 1 5 10 15

Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Met
 35 40

<210> 63
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP4 (43 a.a.)

<400> 63

Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
 1 5 10 15

Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
 20 25 30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
 35 40

<210> 64
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP4 (44 a.a.)

<400> 64

Gln Gln Val Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
 1 5 10 15

Val Thr Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
 35 40

<210> 65
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP4 (120 n.a.)

<400> 65
 caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag 60
 cagtaccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg 120

<210> 66
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse TCAP4 (123 n.a.)

<400> 66
 cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc 60
 gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag 120
 atg 123

<210> 67
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP4 (129 n.a.)

<400> 67
 caggtgctga acacggggcg ggtgcaaggc tacgacggct tctttgtgac ctcggtcgag 60
 cagtaccag aactgtcaga cagcgccaac aatatccact tcatgagaca gagcgagatg 120
 ggccgaagg 129

<210> 68
 <211> 132

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Mouse preTCAP4 (132 n.a.)

<400> 68
 cagcaggtgc tgaacacggg gcgggtgcaa ggctacgacg gcttctttgt gacctcggtc 60
 gagcagtacc cagaactgtc agacagcgcc aacaatatcc acttcatgag acagagcgag 120
 atggggccgaa gg 132

<210> 69
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCAP1 (40 a.a.)

<400> 69
 Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
 1 5 10 15
 Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
 20 25 30
 His Phe Met Arg Gln Ser Glu Ile
 35 40

<210> 70
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCAP1 (41 a.a.)

<400> 70
 Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
 1 5 10 15
 Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
 20 25 30
 Ile His Phe Met Arg Gln Ser Glu Ile
 35 40

<210> 71
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human preTCAP1 (43 a.a.)

<400> 71

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
 1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
 20 25 30

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
 35 40

<210> 72
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human preTCAP1 (44 a.a.)

<400> 72

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
 1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
 35 40

<210> 73
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human TCAP1 (120 n.a.)

<400> 73
 cagcttttga gcactgggcg ggtacaaggt tacgatgggt attttgtttt gtctgttgag

cagtatttag aactttctga cagtgccaat aatattcact ttatgagaca gagcgaaata 120

<210> 74
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human TCAP1 (123 n.a.)

<400> 74
 cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtattttgt tttgtctgtt 60
 gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa 120
 ata 123

<210> 75
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human preTCAP1 (129 n.a.)

<400> 75
 cagcttttga gcaactgggcg ggtacaaggt tacgatgggt attttgtttt gtctgttgag 60
 cagtatttag aactttctga cagtgccaat aatattcact ttatgagaca gagcgaaata 120
 ggcaggagg 129

<210> 76
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human preTCAP1 (132 n.a.)

<400> 76
 cagcagcttt tgagcactgg gcgggtacaa ggttacgatg ggtattttgt tttgtctgtt 60
 gagcagtatt tagaactttc tgacagtgcc aataatattc actttatgag acagagcgaa 120
 ataggcagga gg 132

<210> 77
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Human TCAP2 (40 a.a.)

<400> 77

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
 1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
 20 25 30

Gln Phe Leu Arg Gln Asn Glu Met
 35 40

<210> 78

<211> 41

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP2 (41 a.a.)

<400> 78

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
 1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
 20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met
 35 40

<210> 79

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Human preTCAP2 (43 a.a.)

<400> 79

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val
 1 5 10 15

Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile
 20 25 30

Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
 35 40

<210> 80
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human preTCAP2 (44 a.a.)

<400> 80

Gln Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr
 1 5 10 15

Val Leu Pro Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn
 20 25 30

Ile Gln Phe Leu Arg Gln Asn Glu Met Gly Lys Arg
 35 40

<210> 81
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human TCAP2 (120 n.a.)

<400> 81
 cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag 60
 caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg 120

<210> 82
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human TCAP2 (123 n.a.)

<400> 82
 cagcagcttc tgagcaccgg gcgcgtgcaa gggtacgagg gatattacgt gcttcccgtg 60
 gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag 120
 atg 123

<210> 83
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human preTCAP2 (129 n.a.)

<400> 83
 cagcttctga gcaccgggcg cgtgcaaggg tacgagggat attacgtgct tcccgtggag 60
 caatacccag agcttgcaga cagtagcagc aacatccagt ttttaagaca gaatgagatg 120
 ggaaagagg 129

<210> 84
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human preTCAP2 (132 n.a.)

<400> 84
 cagcagcttc tgagcaccgg gcgcgtgcaa gggtagcagg gatattacgt gcttcccgtg 60
 gagcaatacc cagagcttgc agacagtagc agcaacatcc agtttttaag acagaatgag 120
 atgggaaaga gg 132

<210> 85
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCAP3 (40 a.a.)

<400> 85

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
 1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
 20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile
 35 40

<210> 86
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCAP3 (41 a.a.)

<400> 86

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
 1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
 20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile
 35 40

<210> 87
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human preTCAP3 (43 a.a.)

<400> 87

Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr Val
 1 5 10 15

Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Ile
 20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
 35 40

<210> 88
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human preTCAP3 (44 a.a.)

<400> 88

Arg Gln Leu Leu Ser Ala Gly Lys Val Gln Gly Tyr Asp Gly Tyr Tyr
 1 5 10 15

Val Leu Ser Val Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn
 20 25 30

Ile Gln Phe Leu Arg Gln Ser Glu Ile Gly Arg Arg
 35 40

<210> 89
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human TCAP3 (120 n.a.)

<400> 89
 cagctgctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag 60
 cagtacccccg agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc 120

<210> 90
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human TCAP3 (123 n.a.)

<400> 90
 cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcggtg 60
 gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag 120
 atc 123

<210> 91
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human preTCAP (129 n.a.)

<400> 91
 cagctgctga gcgccggcaa ggtgcagggc tacgacgggt actacgtact ctcggtggag 60
 cagtacccccg agctggccga cagcgccaac aacatccagt tcctgcggca gagcgagatc 120
 ggcaggagg 129

<210> 92
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human preTCAP3 (132 n.a.)

<400> 92
 cggcagctgc tgagcgccgg caaggtgcag ggctacgacg ggtactacgt actctcggtg 60
 gagcagtacc ccgagctggc cgacagcgcc aacaacatcc agttcctgcg gcagagcgag 120
 atcggcagga gg 132

<210> 93
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCAP4 (40 a.a.)

<400> 93
 Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
 1 5 10 15
 Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
 20 25 30
 His Phe Met Arg Gln Ser Glu Met
 35 40

<210> 94
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human TCAP4 (41 a.a.)

<400> 94
 Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
 1 5 10 15
 Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Met
 35 40

<210> 95
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human preTCAP4 (43 a..a)

<400> 95

Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe Val
 1 5 10 15

Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn Ile
 20 25 30

His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
 35 40

<210> 96
 <211> 44
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human preTCAP4 (44 a.a.)

<400> 96

Gln Gln Val Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Phe Phe
 1 5 10 15

Val Ile Ser Val Glu Gln Tyr Pro Glu Leu Ser Asp Ser Ala Asn Asn
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Met Gly Arg Arg
 35 40

<210> 97
 <211> 120
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human TCAP4 (120 n.a.)

<400> 97
 cagggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag 60
 cagtacccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg 120

<210> 98
 <211> 123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human TCAP4 (123 n.a.)

<400> 98
 cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc 60
 gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag 120
 atg 123

<210> 99
 <211> 129
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human preTCAP4 (129 n.a.)

<400> 99
 cagggtgctga gcacagggcg ggtgcaaggc tacgacggct ttttcgtgat ctctgtcgag 60
 cagtacccag aactgtcaga cagcgccaac aacatccact tcatgagaca gagcgagatg 120
 ggccggagg 129

<210> 100
 <211> 132
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human preTCAP4 (132 n.a.)

<400> 100
 cagcaggtgc tgagcacagg gcgggtgcaa ggctacgacg gctttttcgt gatctctgtc 60
 gagcagtacc cagaactgtc agacagcgcc aacaacatcc acttcatgag acagagcgag 120
 atgggccgga gg 132

<210> 101
 <211> 41

<212> PRT
 <213> Artificial Sequence

<220>
 <223> G. gallus TCAP-1

<400> 101

Gln Gln Leu Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe
 1 5 10 15

Val Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn
 20 25 30

Ile His Phe Met Arg Gln Ser Glu Ile
 35 40

<210> 102
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Zebrafish TCAP-4

<400> 102

Gln Gln Leu Leu Ser Ser Gly Arg Val Gln Gly Tyr Glu Gly Phe Tyr
 1 5 10 15

Ile Val Ser Val Asp Gln Phe Pro Glu Leu Thr Asp Asn Ile Asn Asn
 20 25 30

Val His Phe Trp Arg Gln Thr Glu Met
 35 40

<210> 103
 <211> 37
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> D. melanogaster Ten-m gene product

<400> 103

Glu Leu Val Gln His Gly Asp Val Asp Gly Trp Asn Gly Asp Ile His
 1 5 10 15

47/77

Ser Ile His Lys Tyr Pro Gln Leu Ala Asp Pro Gly Asn Val Ala Phe
20 25 30

Gln Arg Asp Ala Lys
35

<210> 104
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Human CRF TCAP like region

<400> 104

Ser Glu Glu Pro Pro Ile Ser Leu Asp Leu Thr Phe His Leu Leu Arg
1 5 10 15

Glu Val Leu Glu Met Ala Arg Ala Glu Gln Leu Ala Gln Gln Ala His
20 25 30

Ser Asn Arg Lys Leu Met Glu Ile Ile
35 40

<210> 105
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Human urocortin TCAP-like region

<400> 105

Asp Asn Pro Ser Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr
1 5 10 15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln
20 25 30

Asn Arg Ile Ile Phe Asp Ser Val
35 40

<210> 106
<211> 38
<212> PRT
<213> Artificial Sequence

<220>

<223> Human urocortin 2 TCAP-like region

<400> 106

Ile	Val	Leu	Ser	Leu	Asp	Val	Pro	Ile	Gly	Leu	Leu	Gln	Ile	Leu	Leu
1				5					10					15	

Glu	Gln	Ala	Arg	Ala	Arg	Ala	Ala	Arg	Glu	Gln	Ala	Thr	Thr	Asn	Ala
			20					25						30	

Arg	Ile	Leu	Ala	Arg	Val
					35

<210> 107

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Human urocortin 3 TCAP-like region

<400> 107

Phe	Thr	Leu	Ser	Leu	Asp	Val	Pro	Thr	Asn	Ile	Met	Asn	Leu	Leu	Phe
1				5					10					15	

Asn	Ile	Ala	Lys	Ala	Lys	Asn	Leu	Arg	Ala	Gln	Ala	Ala	Ala	Asn	Ala
			20					25						30	

His	Leu	Met	Ala	Gln	Ile
					35

<210> 108

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> L. migratoria DP

<400> 108

Met	Gly	Met	Gly	Pro	Ser	Leu	Ser	Ile	Val	Asn	Pro	Met	Asp	Val	Leu
1				5					10					15	

Arg	Gln	Arg	Leu	Leu	Leu	Glu	Ile	Ala	Arg	Arg	Arg	Leu	Arg	Asp	Ala
			20					25						30	

Glu Glu Gln Ile Lys Ala Asn Lys Asp Phe Leu Gln Gln Ile
 35 40 45

<210> 109
 <211> 46
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A. domesticus DP

<400> 109

Thr Gly Ala Gln Ser Leu Ser Ile Val Ala Pro Leu Asp Val Leu Arg
 1 5 10 15

Gln Arg Leu Met Asn Glu Leu Asn Arg Arg Arg Met Arg Glu Leu Gln
 20 25 30

Gly Ser Arg Ile Gln Gln Asn Arg Gln Leu Leu Thr Ser Ile
 35 40 45

<210> 110
 <211> 39
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> T. molitor DP

<400> 110

Ser Pro Thr Ile Ser Ile Thr Ala Pro Ile Asp Val Leu Arg Lys Thr
 1 5 10 15

Trp Glu Gln Glu Arg Ala Arg Lys Gln Met Val Ala Gln Asn Asn Arg
 20 25 30

Glu Phe Leu Asn Ser Leu Asn
 35

<210> 111
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>

<223> M. sexta DP-1

<400> 111

Arg Met Pro Ser Leu Ser Ile Asp Leu Pro Met Ser Val Leu Arg Gln
1 5 10 15

Lys Leu Ser Leu Glu Lys Glu Arg Lys Val His Ala Leu Arg Ala Ala
20 25 30

Ala Asn Arg Asn Phe Leu Asn Asp Ile
35 40

<210> 112

<211> 30

<212> PRT

<213> Artificial Sequence

<220>

<223> M. sexta DP-II

<400> 112

Ser Leu Ser Val Asn Pro Ala Val Asp Ile Leu Gln His Arg Tyr Met
1 5 10 15

Glu Lys Val Ala Gln Asn Asn Arg Asn Phe Leu Asn Arg Val
20 25 30

<210> 113

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> P. Americana

<400> 113

Thr Gly Ser Gly Pro Ser Leu Ser Ile Val Asn Pro Leu Asp Val Leu
1 5 10 15

Arg Gln Arg Leu Leu Leu Glu Ile Ala Arg Arg Arg Met Arg Gln Ser
20 25 30

Gln Asp Gln Ile Gln Asn Arg Glu Ile Leu Gln Thr Ile
35 40 45

<210> 114
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> O. keta CRP

<400> 114

Ser Asp Asp Pro Pro Ile Ser Leu Asp Leu Thr Phe His Met Leu Arg
 1 5 10 15

Gln Met Asn Glu Met Ser Arg Ala Glu Gln Leu Gln Gln Gln Ala His
 20 25 30

Ser Asn Arg Lys Met Met Glu Ile Phe
 35 40

<210> 115
 <211> 40
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> R. norvegicus

<400> 115

Asp Asp Pro Pro Leu Ser Ile Asp Leu Thr Phe His Leu Leu Arg Thr
 1 5 10 15

Leu Leu Glu Leu Ala Arg Thr Gln Ser Gln Arg Glu Arg Ala Glu Gln
 20 25 30

Asn Arg Ile Ile Phe Asp Ser Val
 35 40

<210> 116
 <211> 37
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> P. sauvageii

<400> 116

Gln Gly Pro Pro Ile Ser Ile Asp Leu Ser Leu Glu Leu Leu Arg Lys
 1 5 10 15

Met Ile Glu Ile Glu Lys Gln Glu Lys Glu Lys Gln Gln Ala Ala Asn
 20 25 30

Asn Arg Leu Leu Leu
 35

<210> 117
 <211> 41
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> C. carpio US

<400> 117

Asn Asp Asp Pro Pro Ile Ser Ile Asp Leu Thr Phe His Leu Leu Arg
 1 5 10 15

Asn Met Ile Glu Met Ala Arg Asn Glu Asn Gln Arg Glu Gln Ala Gly
 20 25 30

Leu Asn Arg Lys Tyr Leu Asp Glu Val
 35 40

<210> 118
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M. Musculus UCN2

<400> 118

Val Ile Leu Ser Leu Asp Val Pro Ile Gly Leu Leu Arg Ile Leu Leu
 1 5 10 15

Glu Gln Ala Arg Tyr Lys Ala Ala Arg Asn Gln Ala Ala Thr Asn Ala
 20 25 30

Gln Ile Leu Ala His Val
 35

<210> 119
 <211> 38

<212> PRT
 <213> Artificial Sequence

<220>
 <223> R. dano UCN2

<400> 119

Leu Thr Leu Ser Leu Asp Val Pro Thr Asn Ile Met Asn Val Leu Phe
 1 5 10 15

Asp Val Ala Lys Ala Lys Asn Leu Arg Ala Lys Ala Ala Glu Asn Ala
 20 25 30

Arg Leu Leu Ala His Ile
 35

<210> 120
 <211> 305
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Hamster 305bp urocortin cDNA probe examples "cloning mRNA"

<400> 120
 attcaccgcc gctcgggata tgagcctgca ggcgagcggc agcgacggga agaccttccg 60
 ctgtccatcg acctcacatt ccacctgcta cggaccctgc tggagatggc ccggacacag 120
 agccaacgcg agcgagcaga gcagaaccga atcataactca acgcggtggg caagtgatcg 180
 gcccggtgtg ggacccccaaa aggctcgacc ctttccccta cctaccccg ggcctgaagtc 240
 acgcgaccga agtcggctta gtcccgcggt gcagcgctc ccagagttac cctgaacaat 300
 cccgc 305

<210> 121
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCAP1 fwd primer

<400> 121

acgtcagtgt tgatgggagg acta 24

<210> 122

<211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> TCAP1 rvs primer

 <400> 122
 cctcctgcct atttcactct gtctcat

27

<210> 123
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCAP2 Fwd primer

<400> 123
 tcgagggcaa ggacacacac tactt

25

<210> 124
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCAP2 rvs primer

<400> 124
 aagaactgga tgttgctgct actgtc

26

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCAP3 fwd primer

<400> 125
 caacaacgcc ttctacctgg agaac

25

<210> 126
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCAP3 rvs primer

<400> 126

tggttggtggc actgtcagcc a 21

<210> 127
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCAP4 fwd primer

<400> 127
 tttgcctcca gtggttccat ctt 23

<210> 128
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCAP4 rvs primer

<400> 128
 tggatattgt tggcgctgtc tgac 24

<210> 129
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Conserved motif between CRF and TCAP I/L S X X (X)-L/V at amino terminus

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> X=I or L

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> X=T or A

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> X=L, I or G

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> X=D, R or K

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> X=L or V

<400> 129

Xaa Ser Xaa Xaa Xaa Xaa
 1 5

<210> 130
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Conserved motif between CRF and TCAP - In middle L/V-L/I-X-V/aliphatic residue

<220>
 <221> MISC_FEATURE
 <222> (1)..(1)
 <223> X=V or L

<220>
 <221> MISC_FEATURE
 <222> (2)..(2)
 <223> X=L, I or F

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> X=E, N, S or P

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> X=M, L Q, I or V

<400> 130

Xaa Xaa Xaa Xaa
 1

<210> 131
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Conserved motif between CRF and TCAP N/I/A-H/basic residue -I/L/F/-aliphatic at carboxy terminus

<220>
 <221> MISC_FEATURE

<222> (2)..(2)
 <223> X=R, A or I

<220>
 <221> MISC_FEATURE
 <222> (3)..(3)
 <223> X=H or basic residues, K, I, R or Q

<220>
 <221> MISC_FEATURE
 <222> (4)..(4)
 <223> X=I, L or F

<400> 131

Asn Xaa Xaa Xaa
 1

<210> 132
 <211> 8964
 <212> DNA
 <213> Mus musculus

<220>
 <221> exon
 <222> (50)..(8197)

<400> 132
 aagttctaag aagccggacc gatgtgcaca gagaaggaat gaaggaagt atg gat gtg 58
 Met Asp Val
 1

aag gaa cgc agg cct tac tgc tcc ttg acc aag agc aga cgg gaa aag 106
 Lys Glu Arg Arg Pro Tyr Cys Ser Leu Thr Lys Ser Arg Arg Glu Lys
 5 10 15

gaa agg cgc tat aca aat tcg tcc gcg gac aat gag gag tgt agg gtc 154
 Glu Arg Arg Tyr Thr Asn Ser Ser Ala Asp Asn Glu Glu Cys Arg Val
 20 25 30 35

ccc acg cag aag tcc tat agt tcc agt gaa acc ttg aaa gct ttc gat 202
 Pro Thr Gln Lys Ser Tyr Ser Ser Ser Glu Thr Leu Lys Ala Phe Asp
 40 45 50

cat gat tat tca cgg ctg ctt tat gga aac aga gta aag gat ttg gtc 250
 His Asp Tyr Ser Arg Leu Leu Tyr Gly Asn Arg Val Lys Asp Leu Val
 55 60 65

cac aga gaa gcc gac gag tat act aga caa gga cag aat ttt acc cta 298
 His Arg Glu Ala Asp Glu Tyr Thr Arg Gln Gly Gln Asn Phe Thr Leu
 70 75 80

agg cag tta gga gtg tgt gaa tcc gca act cga aga gga gtg gca ttc 346
 Arg Gln Leu Gly Val Cys Glu Ser Ala Thr Arg Arg Gly Val Ala Phe

85	90	95	
tgt gcg gaa atg ggg ctc cct cac aga ggt tac tcc atc agt gca ggg			394
Cys Ala Glu Met Gly Leu Pro His Arg Gly Tyr Ser Ile Ser Ala Gly			
100	105	110	115
tca gat gcg gat acg gaa aac gaa gca gtg atg tcc cct gag cat gcc			442
Ser Asp Ala Asp Thr Glu Asn Glu Ala Val Met Ser Pro Glu His Ala			
	120	125	130
atg aga ctt tgg ggc agg ggg gtc aaa tcg ggc cgc agt tcc tgc ctg			490
Met Arg Leu Trp Gly Arg Gly Val Lys Ser Gly Arg Ser Ser Cys Leu			
	135	140	145
tca agc cgg tcc aac tcc gcc ctc acc ctg aca gac acg gag cac gag			538
Ser Ser Arg Ser Asn Ser Ala Leu Thr Leu Thr Asp Thr Glu His Glu			
	150	155	160
aac agg tcg gac agt gag agc gag caa cct tca aac aac cca ggg caa			586
Asn Arg Ser Asp Ser Glu Ser Glu Gln Pro Ser Asn Asn Pro Gly Gln			
	165	170	175
ccc acc ctg cag cct ttg ccg cca tcc cac aag cag cac ccg gcg cag			634
Pro Thr Leu Gln Pro Leu Pro Pro Ser His Lys Gln His Pro Ala Gln			
	180	185	190
cat cac ccg tcc atc act tcc ctc aat aga aac tcc ctg acc aat aga			682
His His Pro Ser Ile Thr Ser Leu Asn Arg Asn Ser Leu Thr Asn Arg			
	200	205	210
agg aac cag agt ccg gcc ccg ccg gct gct ttg ccc gcc gag ctg caa			730
Arg Asn Gln Ser Pro Ala Pro Pro Ala Ala Leu Pro Ala Glu Leu Gln			
	215	220	225
acc aca ccc gag tcc gtc cag ctg cag gac agc tgg gtc ctt ggc agt			778
Thr Thr Pro Glu Ser Val Gln Leu Gln Asp Ser Trp Val Leu Gly Ser			
	230	235	240
aat gta cca ctg gaa agc agg cat ttc cta ttc aaa aca ggg aca ggg			826
Asn Val Pro Leu Glu Ser Arg His Phe Leu Phe Lys Thr Gly Thr Gly			
	245	250	255
acg acg cca ctg ttc agt acg gca acc ccg gga tac aca atg gca tct			874
Thr Thr Pro Leu Phe Ser Thr Ala Thr Pro Gly Tyr Thr Met Ala Ser			
	260	265	270
ggc tct gtt tat tct ccg cct acc cgg cca ctt cct aga aac acc cta			922
Gly Ser Val Tyr Ser Pro Pro Thr Arg Pro Leu Pro Arg Asn Thr Leu			
	280	285	290
tca aga agt gct ttt aaa ttc aag aag tct tca aag tac tgc agc tgg			970
Ser Arg Ser Ala Phe Lys Phe Lys Lys Ser Ser Lys Tyr Cys Ser Trp			
	295	300	305
agg tgc acc gca ctg tgt gct gta ggg gtc tca gtg ctc ctg gcc att			1018
Arg Cys Thr Ala Leu Cys Ala Val Gly Val Ser Val Leu Leu Ala Ile			

310	315	320	
ctc ctc tcc tat ttt ata gca atg cat cta ttt ggc ctc aac tgg cac Leu Leu Ser Tyr Phe Ile Ala Met His Leu Phe Gly Leu Asn Trp His 325 330 335			1066
tta cag cag acg gaa aat gac aca ttc gag aat gga aaa gtg aat tct Leu Gln Gln Thr Glu Asn Asp Thr Phe Glu Asn Gly Lys Val Asn Ser 340 345 350 355			1114
gac acc gtg cca aca aac act gta tcg tta cct tct ggc gac aat gga Asp Thr Val Pro Thr Asn Thr Val Ser Leu Pro Ser Gly Asp Asn Gly 360 365 370			1162
aaa tta ggt gga ttt aca cat gaa aat aac acc ata gat tcc gga gaa Lys Leu Gly Gly Phe Thr His Glu Asn Asn Thr Ile Asp Ser Gly Glu 375 380 385			1210
ctt gat att ggc cgg aga gca att caa gag gtt ccc ccc ggg atc ttc Leu Asp Ile Gly Arg Arg Ala Ile Gln Glu Val Pro Pro Gly Ile Phe 390 395 400			1258
tgg aga tcg cag ctc ttt att gat cag cca cag ttt ctt aag ttc aac Trp Arg Ser Gln Leu Phe Ile Asp Gln Pro Gln Phe Leu Lys Phe Asn 405 410 415			1306
atc tct ctt cag aag gat gca ttg atc gga gtg tac ggc cgg aag ggc Ile Ser Leu Gln Lys Asp Ala Leu Ile Gly Val Tyr Gly Arg Lys Gly 420 425 430 435			1354
tta ccg cct tcc cat act cag tac gac ttt gtg gaa cta ctg gat ggt Leu Pro Pro Ser His Thr Gln Tyr Asp Phe Val Glu Leu Leu Asp Gly 440 445 450			1402
agc agg tta att gcg aga gag cag cgg aac ctg gtg gag tcc gaa aga Ser Arg Leu Ile Ala Arg Glu Gln Arg Asn Leu Val Glu Ser Glu Arg 455 460 465			1450
gcc ggg cgg cag gcg aga tct gtc agc ctg cac gaa gct ggc ttc atc Ala Gly Arg Gln Ala Arg Ser Val Ser Leu His Glu Ala Gly Phe Ile 470 475 480			1498
cag tac ttg gat tct gga atc tgg cat ctg gct ttt tat aac gac ggg Gln Tyr Leu Asp Ser Gly Ile Trp His Leu Ala Phe Tyr Asn Asp Gly 485 490 495			1546
aaa aac cca gag cag gtc tcc ttt aac acg atc gtt ata gag tct gtg Lys Asn Pro Glu Gln Val Ser Phe Asn Thr Ile Val Ile Glu Ser Val 500 505 510 515			1594
gtg gaa tgc ccc cga aat tgc cat gga aat gga gag tgt gtt tct gga Val Glu Cys Pro Arg Asn Cys His Gly Asn Gly Glu Cys Val Ser Gly 520 525 530			1642
act tgc cat tgt ttc ccc ggg ttt cta ggt ccg gat tgt tca aga gca Thr Cys His Cys Phe Pro Gly Phe Leu Gly Pro Asp Cys Ser Arg Ala			1690

535	540	545	
gcc tgt ccg gtg ctc tgt agt ggc aac ggg caa tac tcc aag ggc cgc Ala Cys Pro Val Leu Cys Ser Gly Asn Gly Gln Tyr Ser Lys Gly Arg 550 555 560			1738
tgc ctg tgc ttc agt ggc tgg aag ggc acc gag tgt gac gtg ccg acg Cys Leu Cys Phe Ser Gly Trp Lys Gly Thr Glu Cys Asp Val Pro Thr 565 570 575			1786
acc cag tgc att gac ccg cag tgc ggg ggt cgt ggg att tgc atc atg Thr Gln Cys Ile Asp Pro Gln Cys Gly Gly Arg Gly Ile Cys Ile Met 580 585 590 595			1834
ggc tct tgc gct tgt aac tcg gga tac aaa gga gaa aac tgt gag gaa Gly Ser Cys Ala Cys Asn Ser Gly Tyr Lys Gly Glu Asn Cys Glu Glu 600 605 610			1882
gcg gac tgt cta gac cct gga tgt tct aat cac ggg gtg tgt atc cat Ala Asp Cys Leu Asp Pro Gly Cys Ser Asn His Gly Val Cys Ile His 615 620 625			1930
ggg gaa tgt cac tgc aat cca ggc tgg ggt ggc agc aac tgt gaa ata Gly Glu Cys His Cys Asn Pro Gly Trp Gly Gly Ser Asn Cys Glu Ile 630 635 640			1978
ctg aag act atg tgt gca gac cag tgc tca ggc cac ggg act tac ctt Leu Lys Thr Met Cys Ala Asp Gln Cys Ser Gly His Gly Thr Tyr Leu 645 650 655			2026
caa gaa agc ggc tcc tgc act tgc gac cca aat tgg act ggc ccc gac Gln Glu Ser Gly Ser Cys Thr Cys Asp Pro Asn Trp Thr Gly Pro Asp 660 665 670 675			2074
tgc tca aat gaa ata tgt tca gtg gac tgc ggc tca cac ggc gtc tgc Cys Ser Asn Glu Ile Cys Ser Val Asp Cys Gly Ser His Gly Val Cys 680 685 690			2122
atg ggg ggc tcc tgt cgc tgt gaa gaa ggc tgg acc ggc ccg gcg tgt Met Gly Gly Ser Cys Arg Cys Glu Glu Gly Trp Thr Gly Pro Ala Cys 695 700 705			2170
aat cag aga gct tgc cac cct cgc tgt gct gag cac ggg acg tgc aag Asn Gln Arg Ala Cys His Pro Arg Cys Ala Glu His Gly Thr Cys Lys 710 715 720			2218
gac ggc aag tgc gag tgc agc caa gga tgg aac gga gag cac tgc aca Asp Gly Lys Cys Glu Cys Ser Gln Gly Trp Asn Gly Glu His Cys Thr 725 730 735			2266
att gct cac tat ttg gat aag ata gtt aaa gag ggt tgc ccc ggc ttg Ile Ala His Tyr Leu Asp Lys Ile Val Lys Glu Gly Cys Pro Gly Leu 740 745 750 755			2314
tgc aac agc aat ggg aga tgc aca ctg gac caa aac ggc tgg cac tgc Cys Asn Ser Asn Gly Arg Cys Thr Leu Asp Gln Asn Gly Trp His Cys			2362

760					765					770						
gtt	tgc	cag	cca	ggg	tgg	aga	gga	gca	ggc	tgt	gac	gta	gcc	atg	gag	2410
Val	Cys	Gln	Pro	Gly	Trp	Arg	Gly	Ala	Gly	Cys	Asp	Val	Ala	Met	Glu	
775					780					785						
acc	ctc	tgt	aca	gac	agc	aaa	gac	aac	gaa	gga	gac	gga	ctc	att	gac	2458
Thr	Leu	Cys	Thr	Asp	Ser	Lys	Asp	Asn	Glu	Gly	Asp	Gly	Leu	Ile	Asp	
790					795					800						
tgc	atg	gat	cct	gat	tgc	tgc	ctc	cag	agc	tcc	tgc	caa	aac	cag	ccc	2506
Cys	Met	Asp	Pro	Asp	Cys	Cys	Leu	Gln	Ser	Ser	Cys	Gln	Asn	Gln	Pro	
805					810					815						
tac	tgt	cgt	ggc	ttg	cct	gat	cct	cag	gat	atc	att	agc	caa	agc	ctt	2554
Tyr	Cys	Arg	Gly	Leu	Pro	Asp	Pro	Gln	Asp	Ile	Ile	Ser	Gln	Ser	Leu	
820					825					830					835	
cag	aca	cca	tct	cag	caa	gct	gcc	aag	tcc	ttc	tat	gac	cga	atc	agt	2602
Gln	Thr	Pro	Ser	Gln	Gln	Ala	Ala	Lys	Ser	Phe	Tyr	Asp	Arg	Ile	Ser	
840					845					850						
ttc	ctg	att	gga	tcg	gat	agc	acc	cac	gtg	ctc	cct	gga	gaa	agt	ccg	2650
Phe	Leu	Ile	Gly	Ser	Asp	Ser	Thr	His	Val	Leu	Pro	Gly	Glu	Ser	Pro	
855					860					865						
ttc	aat	aag	agt	ctt	gcg	tcc	gtc	atc	aga	ggc	caa	gta	cta	aca	gct	2698
Phe	Asn	Lys	Ser	Leu	Ala	Ser	Val	Ile	Arg	Gly	Gln	Val	Leu	Thr	Ala	
870					875					880						
gat	gga	acc	cca	ctt	att	ggc	gtc	aac	gtg	tcg	ttt	tta	cac	tac	tcg	2746
Asp	Gly	Thr	Pro	Leu	Ile	Gly	Val	Asn	Val	Ser	Phe	Leu	His	Tyr	Ser	
885					890					895						
gaa	tat	gga	tat	acc	att	acc	cgc	cag	gat	gga	atg	ttt	gac	ttg	gtg	2794
Glu	Tyr	Gly	Tyr	Thr	Ile	Thr	Arg	Gln	Asp	Gly	Met	Phe	Asp	Leu	Val	
900					905					910					915	
gca	aat	ggt	ggc	gct	tct	ctg	act	ttg	gta	ttt	gag	cgt	tcc	cca	ttc	2842
Ala	Asn	Gly	Gly	Ala	Ser	Leu	Thr	Leu	Val	Phe	Glu	Arg	Ser	Pro	Phe	
920					925					930						
ctc	act	cag	tac	cac	act	gtg	tgg	att	ccc	tgg	aat	gtc	ttt	tat	gtg	2890
Leu	Thr	Gln	Tyr	His	Thr	Val	Trp	Ile	Pro	Trp	Asn	Val	Phe	Tyr	Val	
935					940					945						
atg	gat	acc	ctt	gtc	atg	aag	aaa	gag	gag	aac	gac	att	ccc	agc	tgt	2938
Met	Asp	Thr	Leu	Val	Met	Lys	Lys	Glu	Glu	Asn	Asp	Ile	Pro	Ser	Cys	
950					955					960						
gac	ctc	agt	ggc	ttt	gtg	agg	cca	agt	ccc	atc	att	gtg	tct	tca	ccg	2986
Asp	Leu	Ser	Gly	Phe	Val	Arg	Pro	Ser	Pro	Ile	Ile	Val	Ser	Ser	Pro	
965					970					975						
tta	tcc	acc	ttc	ttc	agg	tct	tcc	cct	gag	gac	agc	ccc	atc	atc	ccc	3034
Leu	Ser	Thr	Phe	Phe	Arg	Ser	Ser	Pro	Glu	Asp	Ser	Pro	Ile	Ile	Pro	

980	985	990	995
gag aca cag gtc ctg Glu Thr Gln Val Leu 1000	cat gaa gaa acc aca His Glu Glu Thr Thr 1005	att cca gga aca gat Ile Pro Gly Thr Asp 1010	3079
ttg aaa ctt tcc tac Leu Lys Leu Ser Tyr 1015	ctg agt tcc aga gcg Leu Ser Ser Arg Ala 1020	gca ggg tac aag tca Ala Gly Tyr Lys Ser 1025	3124
gtt ctt aag att acc Val Leu Lys Ile Thr 1030	atg acc cag gcc gtc Met Thr Gln Ala Val 1035	ata ccg ttt aac ctc Ile Pro Phe Asn Leu 1040	3169
atg aag gtc cat ctg Met Lys Val His Leu 1045	atg gtg gcc gtg gtt Met Val Ala Val Val 1050	ggg aga ctc ttc cag Gly Arg Leu Phe Gln 1055	3214
aag tgg ttt cct gcc Lys Trp Phe Pro Ala 1060	tcg cca aac ttg gcc Ser Pro Asn Leu Ala 1065	tac acg ttc atc tgg Tyr Thr Phe Ile Trp 1070	3259
gat aag acg gac gca Asp Lys Thr Asp Ala 1075	tat aat cag aaa gtc Tyr Asn Gln Lys Val 1080	tac ggc ttg tca gag Tyr Gly Leu Ser Glu 1085	3304
gca gtt gtg tcc gtc Ala Val Val Ser Val 1090	gga tac gag tac gag Gly Tyr Glu Tyr Glu 1095	tcg tgc ttg gac ctg Ser Cys Leu Asp Leu 1100	3349
act ctc tgg gaa aag Thr Leu Trp Glu Lys 1105	agg act gcc gtt ttg Arg Thr Ala Val Leu 1110	caa ggc tat gag ttg Gln Gly Tyr Glu Leu 1115	3394
gat gct tcg aac atg Asp Ala Ser Asn Met 1120	ggc ggc tgg acg ttg Gly Gly Trp Thr Leu 1125	gac aag cac cat gta Asp Lys His His Val 1130	3439
ctg gac gtt cag aac Leu Asp Val Gln Asn 1135	ggc ata cta tac aaa Gly Ile Leu Tyr Lys 1140	gga aat gga gaa aat Gly Asn Gly Glu Asn 1145	3484
cag ttc atc tct cag Gln Phe Ile Ser Gln 1150	cag cct ccg gtg gtc Gln Pro Pro Val Val 1155	agc agc atc atg ggt Ser Ser Ile Met Gly 1160	3529
aat ggt cgg agg cgt Asn Gly Arg Arg Arg 1165	agc atc tca tgc cca Ser Ile Ser Cys Pro 1170	agt tgc aat ggt caa Ser Cys Asn Gly Gln 1175	3574
gct gac ggg aac aaa Ala Asp Gly Asn Lys 1180	ctc ctg gca ccc gtg Leu Leu Ala Pro Val 1185	gcg ctt gcc tgt ggg Ala Leu Ala Cys Gly 1190	3619
atc gac ggc agt cta Ile Asp Gly Ser Leu 1195	tac gta ggg gat ttc Tyr Val Gly Asp Phe 1200	aat tac gtc cgg cgg Asn Tyr Val Arg Arg 1205	3664

1195					1200					1205					
ata	ttc	ccg	tct	ggg	aat	gtg	aca	agt	gtt	tta	gaa	cta	aga	aat	3709
Ile	Phe	Pro	Ser	Gly	Asn	Val	Thr	Ser	Val	Leu	Glu	Leu	Arg	Asn	
				1210					1215					1220	
aaa	gat	ttt	aga	cat	agt	agc	aac	cca	gct	cac	aga	tac	tac	ctg	3754
Lys	Asp	Phe	Arg	His	Ser	Ser	Asn	Pro	Ala	His	Arg	Tyr	Tyr	Leu	
				1225					1230					1235	
gct	acg	gac	cca	gtc	acc	gga	gat	ttg	tac	gtc	tct	gat	act	aac	3799
Ala	Thr	Asp	Pro	Val	Thr	Gly	Asp	Leu	Tyr	Val	Ser	Asp	Thr	Asn	
				1240					1245					1250	
acc	cgc	aga	atc	tat	cgg	ccg	aaa	tca	ctc	acg	gga	gcc	aaa	gac	3844
Thr	Arg	Arg	Ile	Tyr	Arg	Pro	Lys	Ser	Leu	Thr	Gly	Ala	Lys	Asp	
				1255					1260					1265	
ctg	act	aaa	aac	gct	gaa	gtg	gtg	gca	ggg	acc	ggg	gaa	cag	tgc	3889
Leu	Thr	Lys	Asn	Ala	Glu	Val	Val	Ala	Gly	Thr	Gly	Glu	Gln	Cys	
				1270					1275					1280	
ctt	ccc	ttt	gac	gag	gcc	agg	tgt	ggg	gat	gga	ggc	aag	gct	gtg	3934
Leu	Pro	Phe	Asp	Glu	Ala	Arg	Cys	Gly	Asp	Gly	Gly	Lys	Ala	Val	
				1285					1290					1295	
gaa	gca	acg	ctc	atg	agt	ccc	aaa	gga	atg	gca	atc	gat	aag	aac	3979
Glu	Ala	Thr	Leu	Met	Ser	Pro	Lys	Gly	Met	Ala	Ile	Asp	Lys	Asn	
				1300					1305					1310	
gga	ctg	atc	tac	ttt	gtt	gat	gga	acc	atg	atc	aga	aag	gtt	gat	4024
Gly	Leu	Ile	Tyr	Phe	Val	Asp	Gly	Thr	Met	Ile	Arg	Lys	Val	Asp	
				1315					1320					1325	
caa	aat	gga	atc	ata	tca	act	ctc	ctg	ggc	tcc	aac	gac	ctc	acg	4069
Gln	Asn	Gly	Ile	Ile	Ser	Thr	Leu	Leu	Gly	Ser	Asn	Asp	Leu	Thr	
				1330					1335					1340	
tca	gct	cga	cct	tta	acc	tgt	gat	act	agc	atg	cat	atc	agc	cag	4114
Ser	Ala	Arg	Pro	Leu	Thr	Cys	Asp	Thr	Ser	Met	His	Ile	Ser	Gln	
				1345					1350					1355	
gtg	cgt	ctg	gaa	tgg	ccc	act	gac	ctc	gcg	atc	aac	ccc	atg	gat	4159
Val	Arg	Leu	Glu	Trp	Pro	Thr	Asp	Leu	Ala	Ile	Asn	Pro	Met	Asp	
				1360					1365					1370	
aac	tcc	atc	tac	gtc	ctg	gat	aat	aac	gta	gtt	tta	cag	atc	act	4204
Asn	Ser	Ile	Tyr	Val	Leu	Asp	Asn	Asn	Val	Val	Leu	Gln	Ile	Thr	
				1375					1380					1385	
gaa	aac	cgt	cag	gtc	cgc	atc	gct	gcc	ggg	cgg	ccc	atg	cac	tgt	4249
Glu	Asn	Arg	Gln	Val	Arg	Ile	Ala	Ala	Gly	Arg	Pro	Met	His	Cys	
				1390					1395					1400	
cag	gtc	cct	gga	gtg	gaa	tac	ccg	gtg	ggg	aag	cac	gcg	gtt	cag	4294
Gln	Val	Pro	Gly	Val	Glu	Tyr	Pro	Val	Gly	Lys	His	Ala	Val	Gln	

1405					1410					1415					
acc	acc	ctg	gag	tca	gcc	acg	gcc	att	gct	gtg	tcc	tac	agc	ggg	4339
Thr	Thr	Leu	Glu	Ser	Ala	Thr	Ala	Ile	Ala	Val	Ser	Tyr	Ser	Gly	
1420					1425					1430					
gtc	ctt	tac	atc	acg	gaa	act	gat	gag	aag	aag	atc	aac	cga	ata	4384
Val	Leu	Tyr	Ile	Thr	Glu	Thr	Asp	Glu	Lys	Lys	Ile	Asn	Arg	Ile	
1435					1440					1445					
agg	cag	gtc	acg	aca	gac	ggg	gag	atc	tcc	tta	gtg	gct	ggg	ata	4429
Arg	Gln	Val	Thr	Thr	Asp	Gly	Glu	Ile	Ser	Leu	Val	Ala	Gly	Ile	
1450					1455					1460					
cct	tcg	gaa	tgt	gac	tgc	aag	aac	gac	gcc	aac	tgt	gac	tgc	tac	4474
Pro	Ser	Glu	Cys	Asp	Cys	Lys	Asn	Asp	Ala	Asn	Cys	Asp	Cys	Tyr	
1465					1470					1475					
caa	agc	gga	gac	ggc	tac	gcc	aaa	gat	gcc	aaa	ctc	aat	gcg	ccg	4519
Gln	Ser	Gly	Asp	Gly	Tyr	Ala	Lys	Asp	Ala	Lys	Leu	Asn	Ala	Pro	
1480					1485					1490					
tcc	tcc	ctg	gcc	gcc	tcg	cca	gat	ggc	act	ctg	tac	att	gca	gat	4564
Ser	Ser	Leu	Ala	Ala	Ser	Pro	Asp	Gly	Thr	Leu	Tyr	Ile	Ala	Asp	
1495					1500					1505					
ctg	gga	aat	atc	agg	atc	cgg	gcc	gtt	tcg	aag	aat	aaa	cct	tta	4609
Leu	Gly	Asn	Ile	Arg	Ile	Arg	Ala	Val	Ser	Lys	Asn	Lys	Pro	Leu	
1510					1515					1520					
ctg	aac	tca	atg	aac	ttt	tac	gaa	gtt	gcc	tct	cca	act	gat	caa	4654
Leu	Asn	Ser	Met	Asn	Phe	Tyr	Glu	Val	Ala	Ser	Pro	Thr	Asp	Gln	
1525					1530					1535					
gag	ctc	tac	atc	ttt	gac	atc	aac	ggt	act	cac	cag	tac	acc	gtg	4699
Glu	Leu	Tyr	Ile	Phe	Asp	Ile	Asn	Gly	Thr	His	Gln	Tyr	Thr	Val	
1540					1545					1550					
agc	ctg	gtc	acg	ggt	gac	tac	cta	tat	aat	ttt	agt	tac	agc	aat	4744
Ser	Leu	Val	Thr	Gly	Asp	Tyr	Leu	Tyr	Asn	Phe	Ser	Tyr	Ser	Asn	
1555					1560					1565					
gac	aat	gac	gtc	acc	gct	gta	act	gac	agc	aat	ggc	aac	acc	ctc	4789
Asp	Asn	Asp	Val	Thr	Ala	Val	Thr	Asp	Ser	Asn	Gly	Asn	Thr	Leu	
1570					1575					1580					
cga	atc	cga	agg	gat	ccg	aat	cgg	atg	ccg	gtg	cgg	gtg	gtg	tct	4834
Arg	Ile	Arg	Arg	Asp	Pro	Asn	Arg	Met	Pro	Val	Arg	Val	Val	Ser	
1585					1590					1595					
cct	gat	aac	cag	gtg	ata	tgg	ttg	acc	ata	ggc	acc	aac	ggg	tgt	4879
Pro	Asp	Asn	Gln	Val	Ile	Trp	Leu	Thr	Ile	Gly	Thr	Asn	Gly	Cys	
1600					1605					1610					
ctg	aaa	agc	atg	acc	gct	cag	ggc	ctg	gaa	ctg	gtt	ttg	ttt	act	4924
Leu	Lys	Ser	Met	Thr	Ala	Gln	Gly	Leu	Glu	Leu	Val	Leu	Phe	Thr	

1615	1620	1625	
tac cat ggc aac agt	ggg ctt tta gcc acc	aaa agt gac gaa act	4969
Tyr His Gly Asn Ser	Gly Leu Leu Ala Thr	Lys Ser Asp Glu Thr	
1630	1635	1640	
gga tgg aca aca ttt	ttt gac tat gac agt	gaa ggt cgc ctg acg	5014
Gly Trp Thr Thr Phe	Phe Asp Tyr Asp Ser	Glu Gly Arg Leu Thr	
1645	1650	1655	
aat gtt acc ttc ccc	act ggg gtg gtt aca	aac ctg cac ggg gac	5059
Asn Val Thr Phe Pro	Thr Gly Val Val Thr	Asn Leu His Gly Asp	
1660	1665	1670	
atg gac aag gct atc	acg gtg gac atc gag	tca tcc agc aga gag	5104
Met Asp Lys Ala Ile	Thr Val Asp Ile Glu	Ser Ser Ser Arg Glu	
1675	1680	1685	
gaa gat gtc agc atc	act tcg aac ttg tcc	tcc atc gat tcc ttc	5149
Glu Asp Val Ser Ile	Thr Ser Asn Leu Ser	Ser Ile Asp Ser Phe	
1690	1695	1700	
tac acc atg gtc caa	gac cag tta aga aac	agt tac cag att ggg	5194
Tyr Thr Met Val Gln	Asp Gln Leu Arg Asn	Ser Tyr Gln Ile Gly	
1705	1710	1715	
tat gat ggc tcc ctt	aga atc ttc tat gcc	agt ggt ctg gac tct	5239
Tyr Asp Gly Ser Leu	Arg Ile Phe Tyr Ala	Ser Gly Leu Asp Ser	
1720	1725	1730	
cac tac cag aca gag	ccc cac gtt ctg gct	ggc acg gcg aat ccc	5284
His Tyr Gln Thr Glu	Pro His Val Leu Ala	Gly Thr Ala Asn Pro	
1735	1740	1745	
aca gta gcc aaa aga	aac atg act ctt ccc	ggg gag aac ggg cag	5329
Thr Val Ala Lys Arg	Asn Met Thr Leu Pro	Gly Glu Asn Gly Gln	
1750	1755	1760	
aat ctg gtg gag tgg	aga ttc cga aaa gaa	caa gcc cag ggc aaa	5374
Asn Leu Val Glu Trp	Arg Phe Arg Lys Glu	Gln Ala Gln Gly Lys	
1765	1770	1775	
gtc aac gta ttc ggc	cgg aag ctc agg gtc	aat ggg cgc aac cta	5419
Val Asn Val Phe Gly	Arg Lys Leu Arg Val	Asn Gly Arg Asn Leu	
1780	1785	1790	
ctc tca gtg gac ttt	gat cgg acc acc aag	acg gaa aag atc tat	5464
Leu Ser Val Asp Phe	Asp Arg Thr Thr Lys	Thr Glu Lys Ile Tyr	
1795	1800	1805	
gat gac cac cgg aaa	ttt ctc ctg agg atc	gct tac gac acg tcg	5509
Asp Asp His Arg Lys	Phe Leu Leu Arg Ile	Ala Tyr Asp Thr Ser	
1810	1815	1820	
ggg cac ccg act ctc	tgg ctg ccg agt agc	aag cta atg gca gtg	5554
Gly His Pro Thr Leu	Trp Leu Pro Ser Ser	Lys Leu Met Ala Val	

				1825					1830					1835								
aac	gtc	acc	tac	tca	tcc	acc	ggt	caa	att	gcc	agc	atc	cag	aga	5599							
Asn	Val	Thr	Tyr	Ser	Ser	Thr	Gly	Gln	Ile	Ala	Ser	Ile	Gln	Arg								
				1840					1845					1850								
ggg	acc	acg	agc	gaa	aag	gtg	gac	tat	gac	agc	cag	ggg	agg	atc	5644							
Gly	Thr	Thr	Ser	Glu	Lys	Val	Asp	Tyr	Asp	Ser	Gln	Gly	Arg	Ile								
				1855					1860					1865								
gta	tct	cgg	gtc	ttt	gcc	gat	ggg	aaa	aca	tgg	agt	tac	acg	tac	5689							
Val	Ser	Arg	Val	Phe	Ala	Asp	Gly	Lys	Thr	Trp	Ser	Tyr	Thr	Tyr								
				1870					1875					1880								
ttg	gaa	aag	tcc	atg	gtt	ctt	ctg	ctc	cat	agc	cag	cgg	cag	tac	5734							
Leu	Glu	Lys	Ser	Met	Val	Leu	Leu	Leu	His	Ser	Gln	Arg	Gln	Tyr								
				1885					1890					1895								
atc	ttc	gaa	tac	gac	atg	tgg	gac	cgc	ctg	tcc	gcc	atc	acc	atg	5779							
Ile	Phe	Glu	Tyr	Asp	Met	Trp	Asp	Arg	Leu	Ser	Ala	Ile	Thr	Met								
				1900					1905					1910								
ccc	agt	gtg	gct	cgc	cac	acc	atg	cag	acc	atc	cgg	tcc	att	ggc	5824							
Pro	Ser	Val	Ala	Arg	His	Thr	Met	Gln	Thr	Ile	Arg	Ser	Ile	Gly								
				1915					1920					1925								
tac	tac	cgc	aac	atc	tac	aat	ccc	cca	gaa	agc	aat	gcc	tct	atc	5869							
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Ile	Thr	Asp	Tyr	Asn	Glu	Glu	Gly	Leu	Leu	Leu	Gln	Thr	Ala	Phe								
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ctg	gga	acg	agt	cgg	agg	gtc	tta	ttc	aag	tat	aga	agg	cag	acc	5959							
Leu	Gly	Thr	Ser	Arg	Arg	Val	Leu	Phe	Lys	Tyr	Arg	Arg	Gln	Thr								
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agg	cta	tca	gaa	att	tta	tac	gac	agc	aca	aga	gtc	agt	ttt	acc	6004							
Arg	Leu	Ser	Glu	Ile	Leu	Tyr	Asp	Ser	Thr	Arg	Val	Ser	Phe	Thr								
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Tyr	Asp	Glu	Thr	Ala	Gly	Val	Leu	Lys	Thr	Val	Asn	Leu	Gln	Ser								
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gat	ggt	ttt	att	tgc	acc	att	aga	tac	agg	caa	att	ggt	ccc	ctg	6094							
Asp	Gly	Phe	Ile	Cys	Thr	Ile	Arg	Tyr	Arg	Gln	Ile	Gly	Pro	Leu								
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Ile	Asp	Arg	Gln	Ile	Phe	Arg	Phe	Ser	Glu	Asp	Gly	Met	Val	Asn								
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Tyr Pro Thr Arg Ile	Thr His Val Tyr Asn	His Ser Ser Ser Glu	
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Ile Thr Ser Leu Tyr	Tyr Asp Leu Gln Gly	His Leu Phe Ala Met	
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Gly Thr Pro Leu Ala	Val Phe Ser Ser Asn	Gly Leu Met Leu Lys	
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Gln Thr Gln Tyr Thr	Ala Tyr Gly Glu Ile	Tyr Phe Asp Ser Asn	
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Pro Leu Thr Lys Leu	Ile His Phe Gly Glu	Arg Asp Tyr Asp Ile	
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Gln Leu Leu Ser Xaa Xaa Lys Val Xaa Gly Tyr Asp Gly Tyr Tyr Val
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Leu Ser Xaa Glu Gln Tyr Pro Glu Leu Ala Asp Ser Ala Asn Asn Xaa
20 25 30

Gln Phe Leu Arg Gln Ser Glu Ile
35 40

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<223> G. gallus TCAP2

<400> 136

Thr Gly Arg Val Gln Gly Tyr Glu Gly Tyr Tyr Val Leu Pro Val Glu
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Gln Tyr Pro Glu Leu Ala Asp Ser Ser Ser Asn Ile Gln Phe Leu Arg
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Gln Asn Glu Met
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Thr Ile Leu Gly Ile Gln Cys Glu Leu Gln Lys Gln Leu Arg Asn Phe
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 20 25 30

Cys Leu Glu Gly Gly Lys Gln Pro Arg Phe Ala Ala Val Pro Ser Val
 35 40 45

Phe Gly Lys Gly Ile Lys Phe Ala Ile Lys Asp Gly Ile Val Thr Ala
 50 55 60

Ile Ile Gly Val Ala Asn Glu Asp Ser Arg Arg Leu Ala Ala Ile Leu
 65 70 75 80

Asn Asn Ala His Tyr Leu Glu Asn Leu His Phe Thr Ile Glu Gly Arg
 85 90 95

Asp Thr His Tyr Phe Ile Lys Leu Gly Ser Leu Glu Glu Asp Leu Val
 100 105 110

77/77

Leu Ile Gly Asn Thr Gly Gly Arg Arg Ile Leu Glu Asn Gly Val Asn
 115 120 125

Val Thr Val Ser Gln Met Thr Ser Val Leu Asn Gly Arg Thr Arg Arg
 130 135 140

Phe Ala Asp Ile Gln Leu Gln His Gly Ala Leu Cys Phe Asn Ile Arg
 145 150 155 160

Tyr Gly Thr Thr Val Glu Glu Glu Lys Asn His Val Leu Glu Ile Ala
 165 170 175

Arg Gln Arg Ala Val Ala Gln Ala Trp Thr Lys Glu Gln Arg Arg Leu
 180 185 190

Gln Glu Gly Glu Glu Gly Ile Arg Ala Trp Thr Glu Gly Glu Lys Gln
 195 200 205

Gln Leu Leu Ser Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
 210 215 220

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
 225 230 235 240

His Phe Met Arg Gln Ser Glu Ile Gly Arg Arg
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<400> 138

Gln Leu Leu Asn Thr Gly Arg Val Gln Gly Tyr Asp Gly Tyr Phe Val
 1 5 10 15

Leu Ser Val Glu Gln Tyr Leu Glu Leu Ser Asp Ser Ala Asn Asn Ile
 20 25 30

His Phe Met Arg Gln Ser Glu Ile
 35 40